

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 23, 2001, 06:11:10 ; Search time 10.2 Seconds
(without alignments)
755.636 Million cell updates/sec

Title: US-09-559-764-1

Perfect score.: 1198

Sequence: 1 IVGGKRRPQPFLASTQN.....VALFRDWIDGVNNGPGPA 225

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

1 number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1198	100.0	251	1	CAP7_HUMAN	P20160 homo sapien
2	772	64.4	219	1	CAP7_PIG	P80015 sus scrofa
3	500	41.7	267	1	ELNE_HUMAN	P08246 homo sapien
4	476.5	39.8	256	1	PRN3_HUMAN	P24158 homo sapien
5	333	27.8	245	1	MCT1_SHEEP	P80931 ovis aries
6	333	27.8	262	1	GRAA_HUMAN	P12544 homo sapien
7	331.5	27.7	226	1	DDN1_BOVIN	P80219 bos taurus
8	331.5	27.7	248	1	TRY1_CHICK	O90627 gallus gall
9	331	27.6	247	1	MCT2_RAT	P00770 rattus norv
10	329.5	27.5	257	1	GRAM_HUMAN	P51124 homo sapien
11	327.5	27.3	248	1	TRY2_CHICK	O90628 gallus gall
12	327	27.3	253	1	CFAD_HUMAN	P00746 homo sapien
13	326	27.2	258	1	GRAK_RAT	P49864 rattus norv
14	325	27.1	246	1	MCT9_MOUSE	O35164 mus musculus
15	325	27.1	245	1	MCTX_MOUSE	O00356 mus musculus
16	323.5	27.0	259	1	CFAD_MOUSE	P03953 mus musculus
17	323	27.0	259	1	CFAD_PIG	P51779 sus scrofa
18	321	26.8	246	1	MCT1_MOUSE	P11034 mus musculus
19	320.5	26.8	261	1	CATG_MOUSE	P28293 mus musculus
20	320	26.7	246	1	MCT4_RAT	P97592 rattus norv
21	320	26.7	248	1	CATG_MOUSE	P08882 mus musculus
22	318.5	26.6	255	1	CATG_HUMAN	P08311 homo sapien
23	317	26.5	246	1	MCT4_MOUSE	P21812 mus musculus
24	315.5	26.3	247	1	GRAB_MOUSE	P04187 mus musculus
25	314	26.2	251	1	MCT3_SHEEP	O46683 ovis aries
26	313.5	26.2	263	1	GRAK_MOUSE	O35205 mus musculus
27	310.5	25.9	261	1	KLK3_MACMU	P33619 macaca mula
28	310	25.9	244	1	MCT2_MOUSE	P15119 mus musculus
29	310	25.9	260	1	MCT1_RAT	P09650 rattus norv
30	309.5	25.8	263	1	CFAD_RAT	P32038 rattus norv
31	309	25.8	248	1	NKPI_RAT	P18291 rattus norv
32	308	25.7	248	1	GRAF_MOUSE	P08883 mus musculus
33	307.5	25.7	251	1	KLKE_HUMAN	O9p0g3 homo sapien

34	306.5	25.6	248	1	MCT8_RAT	P97594 rattus norv
35	306.5	25.6	264	1	GRAK_HUMAN	P49863 homo sapien
36	306	25.5	254	1	KLK4_HUMAN	O9V5K2 homo sapien
37	305.5	25.5	244	1	TRY2_XENLA	P70059 xenopus lae
38	305.5	25.5	261	1	KLK3_HUMAN	P07288 homo sapien
39	304.5	25.4	238	1	TRY3_SALSA	P35033 salmo salar
40	304.5	25.3	239	1	KLK2_CAVPO	P12323 cavia porce
41	303.5	25.3	250	1	TRYP_PLEPL	P35034 pleuronecte
42	303.5	25.3	260	1	KLK8_HUMAN	O60259 homo sapien
43	303	25.3	246	1	GRAH_HUMAN	P20718 homo sapien
44	303	25.3	248	1	GRL1_RAT	O06605 rattus norv
45	302.5	25.3	260	1	GRAA_MOUSE	P11032 mus musculu

ALIGNMENTS

RESULT	1
CAP7_HUMAN	
ID	CA7_HUMAN
AC	P20160: P80014; STANDARD; PRT; 251 AA.
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-OCT-1993 (Rel. 27, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	AZUROCIDIN PRECURSOR (CATIONIC ANTIMICROBIAL PROTEIN CAP37)
DE	(HEPARIN-BINDING PROTEIN) (HBP).
GN	AZU1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92013155; PubMed=1919011;
RA	Morgan J.G., Sukienicki T., Pereira H.A., Spitznagel J.K.,
RA	Guerra M.E., Larrick J.L.;
RT	"Cloning of the cDNA for the serine protease homolog
RT	CAP37/azurocidin, a microbicidal and chemotactic protein from human
RT	granulocytes.";
RL	J. Immunol. 147:3210-3214(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92390417; PubMed=1518849;
RA	Zimmer M., Medcalf R.L., Fink T.M., Mattmann C., Lichter P.,
RA	Jenne D.E.;
RT	"Three human elastase-like genes coordinately expressed in the
RT	myelomonocyte lineage are organized as a single genetic locus on
RT	19pter.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:8215-8219(1992).
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA	Burkhardt-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA	Danagan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA	Liu S., Attix C., Andrise T., Frankheim M., Amico-Keller G.,
RA	Koefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA	Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Frong S.,
RA	Kobayashi A., Olsen A.S., Carrano A.V.;
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE OF 3-251 FROM N.A.
RC	TISSUE-Neutrophils;
RX	MEDLINE=91264832; PubMed=2049091;
RA	Almeida R.P., Melchior M., Campanelli D., Nathan C., Gabay J.E.;
RT	"Complementary DNA sequence of human neutrophil azurocidin, an
RT	antibiotic with extensive homology to serine proteases.";
RL	Biochem. Biophys. Res. Commun. 177:688-695(1991).
RN	[5]
RP	SEQUENCE OF 27-248.
RX	MEDLINE=91032128; PubMed=2226832;
RA	Pohl J., Ferreira H.A., Martin N.M., Spitznagel J.K.;
RT	"Amino acid sequence of CAP37, a human neutrophil granule-derived

RT antibacterial and monocyte-specific chemotactic glycoprotein
 RT structurally similar to neutrophil elastase."
 RL FEBS Lett. 272:200-204(1990).
 RN [16]
 RC SEQUENCE OF 27-248.
 RP TISSUE-Neutrophils;
 RX MEDLINE=91224149; PubMed=2026172;
 RA Flodgaard H., Oestergaard E., Bayne S., Jendensen A., Thomsen J.,
 RA Engels M., Wollmer A.;
 RT "Covalent structure of two novel neutrophil leucocyte-derived
 RT proteins of porcine and human origin. Neutrophil elastase homologues
 RT with strong monocyte and fibroblast chemotactic activities."
 RL Eur. J. Biochem. 197:535-547(1991).
 RN [17]
 RP SEQUENCE OF 27-47.
 RX MEDLINE=91378304; PubMed=1897955;
 RA Green B.G., Weston H., Ashe B.M., Doherty J., Finke P., Hagemann W.,
 RA Lark M., Mao J., Maycock A., Moore V., Rufford R., Shah S.,
 RA Walakavits L., Knight W.B.;
 RT "PMN elastases: a comparison of the specificity of human isozymes and
 RT the enzyme from other species toward substrates and inhibitors."
 RL Arch. Biochem. Biophys. 286:284-292(1991).
 RN [18]
 RP SEQUENCE OF 27-46.
 RX MEDLINE=89315847; PubMed=2501794;
 RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
 RA Marra M.N., Seeger M., Nathan C.F.;
 RT "Antibiotic proteins of human polymorphonuclear leukocytes."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
 RN [19]
 RP SEQUENCE OF 27-46 AND 194-217.
 RX MEDLINE=90130450; PubMed=2404977;
 RA Wilde C.G., Snable J.L., Griffith J.E., Scott R.W.;
 RT "Characterization of two azurophilic granule proteases with active-site
 RT homology to neutrophil elastase."
 RL J. Biol. Chem. 265:2038-2041(1990).
 RN [10]
 RP SEQUENCE OF 27-67.
 RX TISSUE-Neutrophils;
 RA MEDLINE=90157837; PubMed=2406527;
 RA Pereira H.A., Spitznagel J.K., Pohl J., Wilson D.E., Morgan J.,
 RA Palings I., Larrick J.W.;
 RT "CAP 37, a 37 kd human neutrophil granule cationic protein shares
 RT homology with inflammatory proteinases."
 RL Life Sci. 46:189-196(1990).
 RN [11]
 RP SEQUENCE OF 27-68.
 RX TISSUE-Neutrophils;
 RA MEDLINE=90237224; PubMed=2332502;
 RA Pereira H.A., Shafer W.M., Pohl J., Marston L.E., Spitznagel J.K.;
 RT "CAP37, a human neutrophil-derived chemotactic factor with monocyte
 RT specific activity."
 RL J. Clin. Invest. 85:1468-1476(1990).
 RN [12]
 RP REVIEW.
 RX MEDLINE=92095171; PubMed=1755383;
 RA Morgan J.G., Pereira H.A., Sukiennicki L., Spitznagel J.K.,
 RA Larrick J.W.;
 RT "Human neutrophil granule cationic protein CAP37 is a specific
 RT macrophage chemotaxin that shares homology with inflammatory
 RT proteinases."
 RL Adv. Exp. Med. Biol. 305:89-96(1991).
 RN [13]
 RP SYNTHESIS OF 46-70.
 RX MEDLINE=93281653; PubMed=8506327;
 RA Pereira H.A., Erdem I., Pohl J., Spitznagel J.K.;
 RT "Synthetic bactericidal peptide based on CAP37: a 37-kDa human
 RT neutrophil granule-associated cationic antimicrobial protein
 RT chemotactic for monocytes."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:4733-4737(1993).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=97249288; PubMed=9095193;

RA Iversen L.F., Kastrup J.S., Bjoern S.E., Rasmussen P.B., Wiberg F.C.,
 RA Flodgaard H.J., Larsen I.K.;
 RT "Structure of HBP, a multifunctional protein with a serine proteinase
 RT fold".
 RL Nat. Struct. Biol. 4:265-268(1997).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (1.12 ANGSTROMS).
 RX MEDLINE=98437573; PubMed=9761855;
 RA Karlsen S., Iversen L.F., Larsen I.K., Flodgaard H.J., Kastrup J.S.;
 RT "Atomic resolution structure of human HBP/CAP37/azurocidin."
 RL Acta Crystallogr. D 54:598-609(1998).
 CC -!- FUNCTION: THIS IS A NEUTROPHIL GRANULE-DERIVED ANTIBACTERIAL AND
 CC MONOCYTE- AND FIBROBLAST-SPECIFIC CHEMOTACTIC GLYCOPROTEIN. BINDS
 CC HEPARIN. THE CYTOTOXIC ACTION IS LIMITED TO MANY SPECIES OF GRAM-
 CC NEGATIVE BACTERIA; THIS SPECIFICITY MAY BE EXPLAINED BY A STRONG
 CC AFFINITY OF THE VERY BASIC N-TERMINAL HALF FOR THE NEGATIVELY
 CC CHARGED LIPOPOLYSACCHARIDES THAT ARE UNIQUE TO THE GRAM-NEGATIVE
 CC BACTERIAL OUTER ENVELOPE. IT MAY PLAY A ROLE IN MEDIATING
 CC RECRUITMENT OF MONOCYTES IN THE SECOND WAVE OF INFLAMMATION.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES OF NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. ELASTASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M96326; AAB59353.1; -;
 CC EMBL; X58794; CAA41601.1; -;
 CC EMBL; AC004799; AAC18957.1; -;
 CC PIR; A46455; TRHAZ;
 CC PIR; A46268; A46268;
 CC PDB; 1AE5; 1I-MAR-98.
 CC PDB; 1A7S; 23-MAR-99.
 CC MEROPS; S01.971; -;
 CC MIM; 162815; -;
 CC InterPro; IPR001254; -;
 CC InterPro; IPR001314; -;
 CC Pfam; PF00089; trypsin, 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
 CC PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
 CC Serine protease homolog; Glycoprotein; Chemotaxis; Antibiotic;
 CC Heparin-binding; Signal; 3D-structure.
 CC SIGNAL 1 26
 CC FT CHAIN 27 248 AZUROCIDIN.
 CC FT PROPEP 249 251 POSSESS ANTIBIOTIC ACTIVITY.
 CC FT DOMAIN 46 70 HYDROPHOBIC.
 CC FT DOMAIN 52 84 N-LINKED (GLCNAC. .) (PARTIAL).
 CC FT CARBOHYD 126 126 N-LINKED (GLCNAC. .).
 CC FT CARBOHYD 140 140 N-LINKED (GLCNAC. .).
 CC FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (PARTIAL).
 CC FT DISULFID 52 68
 CC FT DISULFID 149 207
 CC FT DISULFID 180 186
 CC FT DISULFID 197 222
 CC FT VARIANT 248 248
 CC FT MUTAGEN 52 52 MISSING (IN 50% OF THE MOLECULES).
 CC FT MUTAGEN 68 68 /FTID=VAR_006496.
 CC FT CONFLICT 36 36 C->S: LOSS OF ANTIBIOTIC ACTIVITY.
 CC FT CONFLICT 130 130 C->S: LOSS OF ANTIBIOTIC ACTIVITY.
 CC FT CONFLICT 130 130 S -> N (IN REF. 6).
 CC SEQUENCE 251 AA; 26885 MW; 22F80D9EBE87DE60 CRC64;

Query Match 100.0%; Score 1198; DB 1; Length 251;
 Best Local Similarity 100.0%; Pred. No. 6.2e-104;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: November 23, 2001, 06:10:39 ; Search time 17.17 seconds
(without alignments)
998.210 Million cell updates/sec

Title: US-09-559-764-1

Perfect score: 1198
Sequence: 1 IGVGRKARPPFPFLASIQN.....VALFRDWIDGVLNPPGPPA 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

T number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1198	100.0	251	1 TRHUAZ	azurocidin precurs
2	772	64.4	219	1 TRPGAZ	azurocidin - pig
3	500	41.7	267	1 ELHUL	leukocyte elastase
4	481.5	40.2	256	1 PRHU3	proteinase 3 (EC 3
5	471.5	39.4	265	2 I48679	neutrophil elastas
6	333	27.8	262	1 A31372	duodenase A (EC 3.4
7	331.5	27.7	226	2 S69370	duodenase - bovine
8	331	27.6	247	1 PRRTG	mast cell proteina
9	329.5	27.5	249	2 A55634	granzyme M (EC 3.4
10	328	27.4	248	2 S43259	granzyme-like prot
11	327.5	27.3	248	2 S55067	trypsin (EC 3.4.21
12	327	27.3	244	2 A34910	mast cell proteina
13	326	27.2	258	2 I56220	trypsin 2 - rat
14	325	27.1	246	1 DBHU	complement factor
15	325	27.0	246	2 A38678	mast cell proteina
16	323.5	27.0	259	1 WMS28	complement factor
17	321	26.8	261	1 A46504	chymase (EC 3.4.21
18	320.5	26.8	261	2 S40162	cathepsin G (EC 3.
19	320	26.7	248	1 PRMSC2	granzyme C (EC 3.4
20	318.5	26.6	255	2 A27122	cathepsin G (EC 3.
21	317	26.5	246	2 B38678	mast cell proteina
22	316	26.4	244	2 S26042	chymase (EC 3.4.21
23	315.5	26.3	247	1 PRMSCL	granzyme B (EC 3.4
24	314.5	26.3	250	2 T01779	trypsin (EC 3.4.21
25	314	26.2	226	2 JE0151	myonase (EC 3.4. -
26	314	26.2	251	2 T10262	mast cell serine p
27	310.5	25.9	261	1 S35711	seminogelase (EC 3
28	310	25.9	244	2 A46721	chymase (EC 3.4.21
29	310	25.9	251	2 JC2125	chymase (EC 3.4.21

30	309.5	25.8	263	1 I55608	complement factor
31	309	25.8	248	2 A43520	natural killer cel
32	308	25.7	248	1 S01007	granzyme F (EC 3.4
33	306.5	25.6	264	2 S65663	granzyme 3 (EC 3.4
34	305.5	25.5	261	1 A32297	seminogelase (EC 3
35	304.5	25.4	238	2 S31779	trypsin (EC 3.4.21
36	303.5	25.3	239	2 A27207	tissue kallikrein
37	303.5	25.3	250	2 S31384	trypsin (EC 3.4.21
38	303	25.3	246	2 A32692	cytotoxic T-lympho
39	303	25.3	248	2 S33755	granzyme-like prot
40	302.5	25.3	257	2 B45061	granzyme A (EC 3.4
41	302.5	25.3	260	2 A45061	granzyme A (EC 3.4
42	300	25.0	232	1 KQPG	tissue kallikrein
43	300	25.0	246	2 S64707	chymase (EC 3.4.21
44	299.5	25.0	243	2 A35871	trypsin (EC 3.4.21
45	297	24.8	242	2 S49489	trypsin (EC 3.4.21

ALIGNMENTS

RESULT 1

TRHUAZ

azurocidin precursor [validated] - human

N:Alternate names: cationic antimicrobial protein CAP37; heparin-binding protein; neu

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence_revision 30-Sep-1993 #text_change 08-Dec-2000

C:Accession: A46268; A46455; S16450; S18520; S12881; S15445; S14738; S39113; A60708;

R:Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Mattmann, C.; Lichter, P.; Jenne, D.E.

Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992

A:Title: Three human elastase-like genes coordinately expressed in the myelomonocyte

A:Reference number: A46268; MUID:923390417

A:Accession: A46268

A:Molecule type: DNA

A:Residues: 1-251 <ZIM>

A:Cross-references: GB:M96326; NID:q179301; PIDN:AAB59353.1; PID:q179302

A:Note: sequence extracted from NCBI backbone (NCBIN:112883, NCBIN:112891, NCBIN:1128

R:Morgan, J.G.; Sukienicki, T.; Pereira, H.A.; Spitznagel, J.K.; Guerra, M.E.; Larri

J. Immunol. 147, 3210-3214, 1991

A:Title: Cloning of the cDNA for the serine protease homolog CAP37/azurocidin, a micr

A:Reference number: A46455; MUID:92013155

A:Accession: A46455

A:Molecule type: mRNA

A:Residues: 1-251 <MOR>

A:Cross-references: GB:M96326; NID:q179301; PIDN:AAB59353.1; PID:q179302

A:Note: sequence extracted from NCBI backbone (NCBIN:60386, NCBI:60395)

R:Almeida, R.P.; Melchior, M.; Campanelli, D.; Nathan, C.; Gabay, J.E.

Biochem. Biophys. Res. Commun. 177, 688-695, 1991

A:Title: Complementary DNA sequence of human neutrophil azurocidin, an antibiotic wit

A:Reference number: S16450; MUID:91264832

A:Accession: S16450

A:Molecule type: mRNA

A:Residues: 3-251 <ALM>

A:Cross-references: EMBL:X58794; NID:g28976; PIDN:CAA41601.1; PID:g28977

A:Accession: S18520

A:Molecule type: protein

A:Residues: 47-51, 'S', 53-59, 'T', 61-62, 'V', 64-87 <AL2>

R:Pohl, J.; Pereira, H.A.; Martin, N.M.; Spitznagel, J.K.

FEBS Lett. 272, 200-204, 1990

A:Title: Amino acid sequence of CAP37, a human neutrophil granule-derived antibacteri

A:Reference number: S12881; MUID:91032128

A:Accession: S12881

A:Molecule type: protein

A:Residues: 27-248 <POH>

R:Flodgaard, H.; Ostergaard, E.; Bayne, S.; Svendsen, A.; Thomsen, J.; Engels, M.; Wo

Eur. J. Biochem. 197, 535-547, 1991

A:Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of po

A:Reference number: S15393; MUID:91224149

A:Accession: S15445

A:Molecule type: protein

A:Residues: 27-129, 'N', 131-247 <FLO>

A:Note: the sequence from Fig. 7 is inconsistent with that from Fig. 6 in having 190-

R:Green, B.G.; Weston, H.; Ashe, B.M.; Doherty, J.; Finke, P.; Hagmann, W.; Lark, M.; Ma Arch. Biochem. Biophys. 286, 284-292, 1991
A:Title: PMN elastases: a comparison of the specificity of human isozymes and the enzyme
A:Reference number: S14736; MUID:91378304
A:Accession: S14738
A:Molecule type: protein
A:Residues: 27-47 <GRE>
R:Gabay, J.E.; Scott, R.W.; Campanelli, D.; Griffith, J.; Wilde, C.; Marra, M.N.; Seeger Proc. Natl. Acad. Sci. U.S.A. 86, 5610-5614, 1989
A:Title: Antibiotic proteins of human polymorphonuclear leukocytes.
A:Reference number: A33913; MUID:89315847
A:Accession: B33913
A:Molecule type: protein
A:Residues: 27-46 <GAB>
R:Perreira, H.A.; Shafer, W.M.; Pohl, J.; Martens, L.E.; Spitznagel, J.K. J. Clin. Invest. 85, 1468-1476, 1990
A:Title: CAP37, a human neutrophil-derived chemotactic factor with monocyte specific activity
A:Reference number: A60708; MUID:90237224
A:Accession: A60708
A:Molecule type: protein
A:Residues: 27-68 <PER>
R:Wojcik, K.R.; Skubitz, K.M.; Gray, B.H. Infect. Immun. 59, 4193-4200, 1991
A:Title: Comparison of granule proteins from human polymorphonuclear leukocytes which are
A:Reference number: A43600; MUID:92040097
A:Accession: B43600
A:Molecule type: protein
A:Residues: 27-48 <WAS>
R: Miyasaki, K.T.; Bodeau, A.L. Infect. Immun. 60, 4973-4975, 1992
A:Title: Human neutrophil azurocidin synergizes with leukocyte elastase and cathepsin G
A:Reference number: A49211; MUID:93014226
A:Accession: A49211
A:Molecule type: protein
A:Residues: 27-46 <MIY>
R:Shellard, J.E.; Leitch, H.A.; Logan, P.M.; McMaster, W.R.; Levy, J.G. Exp. Hematol. 19, 136-142, 1991
A:Title: Purification of an in vitro inhibitor of normal myelopoiesis using a monoclonal
A:Reference number: A61502; MUID:91122218
A:Accession: A61502
A:Molecule type: protein
A:Residues: 27-48 <SHE>
R:Willde, C.G.; Snable, J.E.; Griffith, J.E.; Scott, R.W. J. Biol. Chem. 265, 2038-2041, 1990
A:Title: Characterization of two azurophilic granule proteases with active-site homology
A:Reference number: A43981; MUID:90130450
A:Accession: B43981
A:Molecule type: protein
A:Residues: 27-35, 'H', 37-46; 194-217 <WIL>
R:Perreira, H.A.; Spitznagel, J.K.; Pohl, J.; Wilson, D.E.; Morgan, J.; Palings, I.; Larr Life Sci. 46, 189-196, 1990
A:Title: CAP 37, a 37 kD human neutrophil granule cationic protein shares homology with
A:Reference number: PH0081; MUID:90157837
A:Accession: PH0081
A:Molecule type: protein
A:Residues: 27-67 <PE2>
A:Experimental source: polymorphonuclear leukocyte
C:Comment: This protein is homologous to several proteinases but lacks proteolytic activity
C:Genetics:
A:Gene: GDB:A291
A:Cross-references: GDB:135033; OMIM:162815
A:Map position: 19p13.3-19p13.3
A:Introns: 20/1; 72/2; 150/3; 198/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; inflammation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-26/Domain: amino-terminal propeptide #status predicted <PRO>
F:27-246/Product: azurocidin #status experimental
F:27-239/Domain: trypsin homology <TRY>
F:67, 115, 201/Region: defective catalytic triad
F:249-251/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:52-68/Disulfide bonds: #status experimental
F:126-140, 171/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:149-207, 180-186, 197-222/Disulfide bonds: #status predicted
Query Match 100.0%; Score 1198; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 6.8e-102;
Matches 225; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 IVGGRKARPPQFPFLASIQNGRHFCCGALIHARFVMTAASCFQSONPGVSTVVLGAYDL 60
DB 27 IVGGRKARPPQFPFLASIQNGRHFCCGALIHARFVMTAASCFQSONPGVSTVVLGAYDL 86
QY 61 RRRERQSRQTFSSMSSENGYDPOONLNDMLQLDREALTSSVTILPLQNATVEAG 120
DB 87 RRRERQSRQTFSSMSSENGYDPOONLNDMLQLDREALTSSVTILPLQNATVEAG 146
QY 121 TRCQVAGWGQSQRSGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRGGICNGDGGTPLV 180
DB 147 TRCQVAGWGQSQRSGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRGGICNGDGGTPLV 206
QY 181 CEGLAHGVASFSGLGPCGPGDPFFTRVALFRDWIDGVLNNPGCPA 225
DB 207 CEGLAHGVASFSGLGPCGPGDPFFTRVALFRDWIDGVLNNPGCPA 251
RESULT 2
TRPGAZ
A:Alternate names: heparin-binding protein
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jul-1997
C:Accession: S15393
R:Flodgaard, H.; Ostergaard, E.; Bayne, S.; Svendsen, A.; Thomsen, J.; Engels, M.; Wo Eur. J. Biochem. 197, 535-547, 1991
A:Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of po
A:Reference number: S15393; MUID:91224149
A:Accession: S15393
A:Molecule type: protein
A:Residues: 1-219 <FLO>
R:Sorensen, H.H.; Thomsen, J.; Bayne, S.; Hojrup, P.; Roepstorff, P. Biomed. Environ. Mass Spectrom. 19, 713-720, 1990
A:Title: Strategies for determination of disulphide bridges in proteins using plasma
A:Reference number: A37448; MUID:91167744
A:Contents: annotation; disulfide bonds
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein
F:1-211/Domain: trypsin homology <TRY>
F:41-88, 173/Region: defective catalytic triad
F:26-42, 122-179, 152-158/Disulfide bonds: #status experimental
F:113, 144/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 64.4%; Score 772; DB 1; Length 219;
Best Local Similarity 68.6%; Pred. No. 4.1e-63;
Matches 151; Conservative 26; Mismatches 41; Indels 2; Gaps 2;
QY 1 IVGGRKARPPQFPFLASIQNGRHFCCGALIHARFVMTAASCFQSONPGVSTVVLGAYDL 60
DB 1 IVGGRRAQPQEPFLASIQNGRHFCCGALIHARFVMTAASCFQSONPGVSTVVLGAYDL 60
QY 61 RRRERQSRQTFSSMSSENGYDPOONLNDMLQLDREALTSSVTILPLQNATVEAG 120
DB 61 ROOE-OSRQTFSSMSSENGYDPOONLNDMLQLDREALTSSVTILPLQNATVEAG 119
QY 121 TRCQVAGWGQSQRSGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRGGICNGDGGTPLV 180
DB 120 TNCQVAGWGQRLRLFRFVNVTVT-SNPCLPDMVICGFSRRGRISQCDRGSTPLV 178
QY 181 CEGLAHGVASFSGLGPCGPGDPFFTRVALFRDWIDGVLNNP 220
DB 179 CNGLAOGVASFLLRRFRSSGFFTRVALFRNWDVSLNPP 218

QY 58 YDLRRERQSRQTSFSSMSNGYDPOONLNDLMEQLDREANLTSSVTILPLPLQNAV 117
 DB 90 HDLSSEPE-QOKFTISQVFNQNNPEENLNDVLAQLNRTASLGKEVAVASLPQDDQTL 148
 QY 118 EAGTRCQVAGWSQSGRLSRFPFRVNTVTPERCRENNYCTGVLTRRGICNGDGGT 177
 DB 149 SQGTQCLAMGWGRGLGTQATPRVLQELNVTVV-TFLCREHNVTLPVRRAGICFGDSGG 207
 QY 178 PLVCEGLAHGVASFSLGPGC--RGPDFFTRVALFRWIDGVNNPGP 222
 DB 208 PLICNGILHGVDSEFVIRECASLOFPDFEFARVSMYQWIONVLRGAEP 254

RESULT 2
 ID Q61096 PRELIMINARY; PRT; 258 AA.
 AC Q61096;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE N-ELASTASE.
 OS Ornithorhynchus anatinus (Duckbill platypus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=129SVJ;
 RC Sturrock A., Franklin K.F., Wu S.Q., Ho J.L., J.R.;
 RT "Characterization and localization of the genes for mouse proteinase-3
 RT and neutrophil elastase."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 2-254 FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=97362044; PubMed=9211743;
 RA Aveskogh M., Lutzeltschwab C., Huang M.R., Hellman L.;
 RT "Characterization of cDNA clones encoding mouse proteinase 3
 RT (myeloblastin) and cathepsin G."
 RL Immunogenetics 46:181-191(1997).
 CC -!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
 CC -!- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
 DR EMBL; AF082186; AAC79701.1; -;
 DR EMBL; U43525; AAB67271.1; -;
 DR HSP; P20160; 1AE5.
 DR MEROPS; S01.134; -;
 DR MGD; MGI:893580; Ptn3.
 DR InterPro; IPR001254; -;
 DR InterPro; IPR001314; -;
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR SMART; SM00020; Tryp_Src; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE . 254 AA; 27626 MW; 00CEB989ACB79CA CRC64;

Query Match 42.6%; Score 510.0; DB 11; Length 254;
 Best Local Similarity 47.1%; Pred. No. 3-42;
 Matches 107; Conservative 35; Mismatches 78; Indels 7; Gaps 4;
 QY 1 IVGGRKARPPFPFLASTQNG--GRHFCGGALXARFVMTAASCFSQNGPVSTVVLGA 57
 DB 30 IVGGEARPHSRPVVASLQSLRFFGSHFCGGLTLPREVLTAACHLQDISQWLVTVVLGA 89
 QY 58 YDLRRERQSRQTSFSSMSNGYDPOONLNDLMEQLDREANLTSSVTILPLPLQNAV 117
 DB 90 HDLSSEPE-QOKFTISQVFNQNNPEENLNDVLAQLNRTASLGKEVAVASLPQDDQTL 148
 QY 118 EAGTRCQVAGWSQSGRLSRFPFRVNTVTPERCRENNYCTGVLTRRGICNGDGGT 177

DB 149 SQGTQCLAMGWGRGLGTQATPRVLQELNVTVV-TFLCREHNVTLPVRRAGICFGDSGG 207
 QY 178 PLVCEGLAHGVASFSLGPGC--RGPDFFTRVALFRWIDGVNNPGP 222
 DB 208 PLICNGILHGVDSEFVIRECASLOFPDFEFARVSMYQWIONVLRGAEP 254
 RESULT 3
 ID Q9GME1 PRELIMINARY; PRT; 258 AA.
 AC Q9GME1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE N-ELASTASE.
 OS Ornithorhynchus anatinus (Duckbill platypus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
 OX NCBI_TaxID=9258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Poorafshar M.M., Hellman L.L.;
 RT "Identification and structural analysis of three serine proteases in a
 RT monotreme, platypus, Ornithorhynchus anatinus."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF275652; AAG00451.1; -;
 SQ SEQUENCE 258 AA; 28165 MW; 2E1752C300A36138 CRC64;

Query Match 39.5%; Score 473.5; DB 6; Length 258;
 Best Local Similarity 47.6%; Pred. No. 4.7e-39;
 Matches 99; Conservative 36; Mismatches 66; Indels 7; Gaps 5;
 QY 13 PFLASIQ-NOGRHFCGGALIHARFVMTAASCFSQNGPVSTVVLGAYDLRRERQSRQTF 71
 DB 35 PYIASLQNRGCGHFCGGTLLHQFVMTAAHCINSRVSRVVLGAHNLRAQE-STRTQY 93
 QY 72 STSSMSNGYDPOONLNDLMEQLDREANLTSSVTILPLPLQNAVTRAGTRCOVAGWSQ 131
 DB 94 SVDQIFENGFSPTLQNDILLVLSRPTLVNANVOLARLPQONQNVSGTGCTCLAMGWG-- 151
 QY 132 RSGRLSRFPFRVNTVTPEDQCRPNNVCTGLTRRGICNGDGGTPLVCEGLAHGVASF 191
 DB 152 KAIMPAAHILQELNVTVV-TNOCORNICTLVPSRRAGICFGDSGGPLVLCNGIVHGIDSF 210
 QY 192 SLGPGCG--PDFFTRVALFRWIDGV 217
 DB 211 VRGGCAGFWPDGFTTRVAQYIQWINSVL 238

RESULT 4
 ID Q61515 PRELIMINARY; PRT; 265 AA.
 AC Q61515;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE NEUTROPHIL ELASTASE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=94309676; PubMed=8035830;
 RA Nuchprayoon I., Meyers S., Scott L.M., Suzow J., Hiebert S.,
 RA Friedman A.D.;
 RT "PEBP2/CBF, the murine homolog of the human myeloid AML1 and PEBP2
 RT beta/CBF beta proto-oncoproteins, regulates the murine myeloperoxidase
 RT and neutrophil elastase genes in immature myeloid cells."
 RL Mol. Cell. Biol. 14:5558-5568(1994).
 CC -!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 23, 2001, 06:10:39 ; Search time 16.8 seconds
(without alignments)
811.928 Million cell updates/sec

Title: US-09-559-764-1

Perfect score: 1198

Sequence: 1 IVGGRKARPPFLASTQN.....VALFRDWIDGLVNNPQGPAA 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

T number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SIDSL1/gcgdata/geneseq/geneseq/AA1980.DAT.*
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21: /SIDSL1/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
1	1198	100.0	225	AA1980	Human heparin-bind
2	1198	100.0	225	AA1981	Mature human hepar
3	1198	100.0	225	AA1982	Human mature hepar
4	1198	100.0	225	AA1983	Human mature hepar
5	1198	100.0	225	AA1984	Human mature hepar
6	1198	100.0	225	AA1985	Human mature hepar
7	1198	100.0	225	AA1986	Human heparin-bind
8	1198	100.0	225	AA1987	Human heparin-bind
9	1198	100.0	225	AA1988	Human pro-heparin
10	1198	100.0	225	AA1989	Human pro-heparin
11	1198	100.0	225	AA1990	Cationic granule p

12	1198	100.0	251	16	AA1984666	Human heparin-bind
13	1198	100.0	251	20	AA198365	Human prepro-hepar
14	1198	100.0	251	21	AA1981878	Human pre-pro hepa
15	1198	100.0	251	22	AA1981894	Human preprohepari
16	1192	99.5	225	21	AA1981881	Human heparin bind
17	1190	99.3	225	21	AA1981883	Human heparin bind
18	1183	98.7	225	21	AA1981882	Human heparin bind
19	1181	98.6	222	14	AA1981935	Recombinant cation
20	1176	98.2	222	14	AA1981935	CAP37 protein. Ho
21	1174	98.0	274	16	AA1984665	Human heparin-bind
22	1173	97.9	221	16	AA1984663	Complete human hep
23	1161	96.9	221	17	AA1984875	Human heparin-bind
24	1161	96.9	221	17	AA1984875	Heparin binding pr
25	930	77.6	197	10	AA1981931	Cationic granule p
26	919.5	76.8	226	12	AA19810669	Porcine heparin-bi
27	772	64.4	239	20	AA1981552	Porcine heparin-bi
28	772	64.4	239	20	AA1981552	Porcine heparin-bi
29	772	64.4	239	20	AA1981552	Porcine heparin-bi
30	772	64.4	239	20	AA1981552	Porcine heparin-bi
31	772	64.4	239	20	AA1981552	Porcine heparin-bi
32	772	64.4	239	20	AA1981552	Porcine heparin-bi
33	772	64.4	239	20	AA1981552	Porcine heparin-bi
34	772	64.4	239	20	AA1981552	Porcine heparin-bi
35	766	63.9	219	17	AA1984876	Complete porcine h
36	765	63.9	219	16	AA1984664	Pig prepro-heparin
37	761.5	63.6	221	20	AA1988119	Heparin binding pr
38	761.5	63.6	221	20	AA1988363	Porcine heparin-bi
39	761.5	63.6	221	22	AA1981892	Mature porcine-hep
40	753	62.9	217	10	AA1980806	Porcine mature hepar
41	500	41.7	247	22	AA1985525	Porcine heparin bi
42	500	41.7	267	9	AA1980335	Human elastase var
43	500	41.7	267	19	AA1984262	Sequence of serine
44	482.5	40.3	265	11	AA19808269	Human neutrophil e
45	482.5	40.3	265	19	AA19808269	Mouse serine prote
						Mouse neutrophil e

ALIGNMENTS

RESULT 1

AA1981551
ID AA1981551 standard; Protein; 225 AA.

AC AA1981551;

DT 03-AUG-1999 (first entry)

XX Human heparin-binding protein (HBP) signal, pro and mature sequence.

DE Heparin-binding protein; HBP; apoptosis; Islets of Langerhans; beta cell;
KW endothelial cell; nerve cell; azurophil granule; chemoattractant; cancer;
KW polymorphonuclear leukocyte; monocyte; neurodegenerative disorder; human;
KW neuromuscular disorder; human immunodeficiency virus; ischemic stroke;
KW proteoglycan; mitochondrial matrix targeting protein; viral infection;
KW apoptosis inhibitor; immune-mediated glomerulonephritis.

OS Homo sapiens.

PN W09926647-A1.

PD 03-JUN-1999.

XX 20-NOV-1998; 98WO-DK00510.

XX 03-DEC-1997; 97DK-0001394.

XX 20-NOV-1997; 97DK-0001324.

PA (NOVO) NOVO-NORDISK AS.

XX Flodgaard HJ;

XX WPI; 1999-347615/29.

DR N-PSDB; AAX60695.

XX Modulating or decreasing apoptosis in cells useful for treating
PT neurodegenerative disorders and neuromuscular disorders
XX Claim 4, 5; Page 12; 74pp; English.
XX The invention relates to a new method of modulating or decreasing
CC apoptosis in mammalian beta cells of islets of Langerhans, endothelial
CC cells or nerve cells. The method comprises administering a mammalian
CC heparin-binding protein (HBP) which in a glycosylated form has: (i) a
CC molecular weight of 28 kDa; (ii) is produced in the azurophilic granules
CC of polymorphonuclear leukocytes; and (iii) is a chemoattractant for
CC monocytes. The new protein is useful for preventing or treating a
CC disorder (preferably in human patients) resulting from apoptosis of
CC mammalian cells, including insufficient functioning of insulin production
CC or insulin action, a neurodegenerative disorder, a neuromuscular
CC disorder, human immunodeficiency virus and ischemic stroke. Compositions
CC (a) comprising HBP and a proteoglycan which binds the HBP; and (b)
CC comprising the HBP and a protein which binds to the HBP are useful for
CC matrix targeting protein and which binds to the HBP are useful for
CC modulating or decreasing apoptosis in mammalian beta cells of islets of
CC Langerhans, endothelial cells or nerve cells. Unlike prior inhibitors,
CC the new apoptosis inhibitor does not cause disorders associated with the
CC inhibition of apoptosis such as cancer, autoimmune disorders such as
CC systemic lupus erythematosus, immune-mediated glomerulonephritis, and
CC viral infections. The present sequence represents the human HBP
CC signal sequence, prosequence and the mature sequence.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1198; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVGGRKARQPFPLASIQNGRHFCCGALIHAREVTAAACFQSONPGVSTVVLGAYDL 60
DB 1 ivggrkarprqpfplasiqnggrhfcgcaliharevtaaacsfqsonpgvstvlgaydl 60
QY 61 RRRERQSRQTFSSISMSSENGYDPOQNLMLQLDREALTSSVTILPLQNAATVEAG 120
DB 61 rrrersqrqtfssissmsengydpqgnldmlqldreanltssvtlplqnatveag 120
QY 121 TRCQVAGWSQSRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRRGICNGDGGTPLV 180
DB 121 trcqvagwsqsrgrlsrfrfvnvtvtpedqcrpnnvctgvltrrgicngdggtplv 180
QY 181 CEGLAGHVASFSLGPCGPGDPFFTRVALFRDWIDGVLNNPQGP 225
DB 181 ceglahgvasfslgpcgpgdpfftrvalfrdwidgvlnnpqp 225

RESULT 2
AAW88118
ID AAW88118 standard; protein; 225 AA.
XX
XX AAW88118;
XX
XX 27-APR-1999 (first entry)
XX Mature human heparin-binding protein.
XX Human; heparin-binding; azurophilic granules; polymorphonuclear leucocyte;
KW chemoattractant; antimicrobial; monocyte macrophage;
KW thrombospondin secretion.
XX Homo sapiens.
OS
XX WO9900417-A1.
PN
XX 07-JAN-1999.
PD
XX 22-JUN-1998; 98WO-DK00275.
PF

XX 22-AUG-1997; 97DK-0000963.
PR 25-JUN-1997; 97US-0082413.
PR 30-JUN-1997; 97DK-0000773.
PR 11-AUG-1997; 97US-0055192.
XX (NOVO) NOVO-NORDISK AS.
PA Bjorn SE, Flodgaard HJ, Rasmussen PB, Svendsen I;
XX Wiberg FC;
XX WPI; 1999-095680/08.
DR N-PSDB; AAX04857.
XX Recombinant eukaryotic cells expressing mammalian heparin binding
PT protein in a mature form - useful as an antimicrobial, a regulator
PT of macrophage or monocyte function, and as a stimulant for monocyte
PT survival
XX Claim 14; Page 7; 59pp; English.
XX The heparin-binding protein is produced by azurophilic granules of
CC polymorphonuclear leucocytes and is a chemoattractant for monocytes.
CC The heparin-binding protein: has antimicrobial activity; regulates
CC monocyte/macrophage function (chemotaxis, survival and differentiation);
CC mediates detachment and contraction of endothelial cells and fibroblasts
CC in monolayer cultures; and stimulates monocyte survival and
CC thrombospondin secretion.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1198; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVGGRKARQPFPLASIQNGRHFCCGALIHAREVTAAACFQSONPGVSTVVLGAYDL 60
DB 1 ivggrkarprqpfplasiqnggrhfcgcaliharevtaaacsfqsonpgvstvlgaydl 60
QY 61 RRRERQSRQTFSSISMSSENGYDPOQNLMLQLDREALTSSVTILPLQNAATVEAG 120
DB 61 rrrersqrqtfssissmsengydpqgnldmlqldreanltssvtlplqnatveag 120
QY 121 TRCQVAGWSQSRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRRGICNGDGGTPLV 180
DB 121 trcqvagwsqsrgrlsrfrfvnvtvtpedqcrpnnvctgvltrrgicngdggtplv 180
QY 181 CEGLAGHVASFSLGPCGPGDPFFTRVALFRDWIDGVLNNPQGP 225
DB 181 ceglahgvasfslgpcgpgdpfftrvalfrdwidgvlnnpqp 225

RESULT 3
AAW88362
ID AAW88362 standard; protein; 225 AA.
XX
XX AAW88362;
XX
XX 26-APR-1999 (first entry)
XX Human mature heparin binding protein.
XX Heparin binding protein; HBP; human; pathogen; Mycobacterium;
KW Listeria; Leishmania; HIV; infection; therapy; mononuclear cell;
KW monocyte; macrophage.
XX Homo sapiens.
OS
XX WO9900416-A1.
PN
XX 07-JAN-1999.
PD
XX

PF 22-JUN-1998; 98WO-DK00274.
 XX 22-AUG-1997; 97DK-0000962.
 PR 25-JUN-1997; 97US-0050787.
 PR 30-JUN-1997; 97DK-0000772.
 XX 11-AUG-1997; 97US-0055191.
 XX (NOVO) NOVO-NORDISK AS.
 XX Flodgaard HJ, Rasmussen PB;
 PI WPI; 1999-095679/08.
 XX N-PSDB; AAX06763.
 DR Inhibiting pathogen entry into mononuclear cells using
 XX heparin-binding protein: useful to treat diseases caused by
 PT intracellular pathogens e.g. Leishmania, Listeria, Mycobacterium
 PT tuberculosis or human immunodeficiency virus
 XX Claim 15; Page 29-30; 57pp; English.

XX This polypeptide comprises human mature heparin binding protein
 CC (HBP). A novel method for inhibiting entry of a pathogen into
 CC mononuclear cells of a patient comprises administering a
 CC pharmaceutical composition comprising a carrier or diluent and a
 CC mammalian HBP, especially a human or porcine HBP (see also AAW88363)
 CC which, in glycosylated form: (i) has mol.wt. of approximately 28
 CC kDa as determined by SDS-PAGE under reducing conditions; (ii) is
 CC produced in the azurophilic granules of polymorphonuclear leukocytes;
 CC and (iii) is a chemotactant for monocytes. The method is useful
 CC for inhibiting the entry of pathogens such as protozoa (especially
 CC Leishmania), bacteria (especially Listeria or Mycobacterium e.g.
 CC Mycobacterium tuberculosis) and viruses (especially HIV) into
 CC mononuclear cells, especially monocytes or macrophages in humans or
 CC pigs. It may also be used to treat diseases caused by intracellular
 CC pathogens.

XX Sequence 225 AA;

Query Match 100.0%; Score 1198; DB 20; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.7e-89;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPRQFPFLASIQNGRHFGGALIHARFVMTAASCFSQNPQGVSTVVLGAYDL 60
 DB 1 ivggrkarprqfpflasiqngrhfgcgali harfvmtaascfsgnpqvstvlgaydl 60
 Q 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAVTEAG 120
 DB 61 rrrerqsrqtfsissmsengydpqnlndmlqldreanltssvtlplqlnatveag 120
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTVPEDQCRPNNVCTGVLTFRGGICNGDGTPLV 180
 DB 121 trcqvagwsqsggrslrfrfvnvtvpedqcrpnnavctgvltrrfggicngdgtplv 180
 QY 181 CEGLAHGVASFLGPGCGRGPDPFFTRVALFRDWIDGVLNPPGPPA 225
 DB 181 ceglahgvasfslgpcgrgpdfftrvalfrdwidgvl nppgppa 225

RESULT 4

AA71876
 ID AAY71876 standard; Protein; 225 AA.
 AC AAY71876;
 XX 26-MAR-2001 (first entry)
 DT Human mature heparin binding protein (HBP).
 XX Human; heparin binding protein; HBP; antiinflammatory; cardiovascular;
 DE immunosuppressive; vasotropic; prevention; treatment; bradykinin;
 KW

KW aprotinin; H-kininogen; systemic inflammatory response syndrome;
 KW pre-kallikrein; ischaemia reperfusion; anaphylaxis; allograft rejection;
 KW adult respiratory distress syndrome; chemoattractant; inflammation;
 XX vascular damage.
 OS Homo sapiens.
 XX WO200066151-A1.
 PN 09-NOV-2000.
 PD 28-APR-2000; 2000WO-DK00213.
 PF 29-APR-1999; 99US-0132748.
 PR 06-MAY-1999; 99DK-0000613.
 PR 01-OCT-1999; 99DK-0001402.
 PR 01-OCT-1999; 99US-0157384.
 XX (NOVO) NOVO NORDISK AS.
 PA Flodgaard HJ, Lindbom L, Bjorn S;
 XX WPI; 2000-687445/67.
 PI N-PSDB; AAD01922.

PT Treating systemic inflammatory response syndrome, ischaemia reperfusion,
 PT anaphylaxis and allograft rejection by modulating release of bradykinin

PS Disclosure; Page 9; 75pp; English.

XX The present sequence is a mature heparin binding protein (HBP) from
 CC human. HBP is a proteolytically inactive protein and is stored in
 CC the azurophilic granules of polymorphonuclear leukocytes. It induces
 CC contraction in the endothelial cells and fibroblasts. It serves as
 CC a chemotactant for monocytes and/or activates them and is involved
 CC in the progression of inflammation. HBP serves as the signalling link
 CC in neutrophil induced vascular damage and activation of contact phase
 CC system with concomitant formation of bradykinin. It specifically plays a
 CC role in the pre-kallikrein (PK) mediated cleavage of H-kininogen (HK) to
 CC obtain the bradykinin sequence. The antagonists of HBP (e.g. aprotinin)
 CC decrease the permeability of the endothelial cells and are used to
 CC prevent or treat disorders resulting from the release of bradykinin
 CC such as systemic inflammatory response syndrome, ischaemia reperfusion,
 CC anaphylaxis and/or allograft rejection. They are also used to treat
 CC adult respiratory distress syndrome.

XX Sequence 225 AA;

Query Match 100.0%; Score 1198; DB 21; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.7e-89;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPRQFPFLASIQNGRHFGGALIHARFVMTAASCFSQNPQGVSTVVLGAYDL 60
 DB 1 ivggrkarprqfpflasiqngrhfgcgali harfvmtaascfsgnpqvstvlgaydl 60
 QY 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAVTEAG 120
 DB 61 rrrerqsrqtfsissmsengydpqnlndmlqldreanltssvtlplqlnatveag 120
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTVPEDQCRPNNVCTGVLTFRGGICNGDGTPLV 180
 DB 121 trcqvagwsqsggrslrfrfvnvtvpedqcrpnnavctgvltrrfggicngdgtplv 180
 QY 181 CEGLAHGVASFLGPGCGRGPDPFFTRVALFRDWIDGVLNPPGPPA 225
 DB 181 ceglahgvasfslgpcgrgpdfftrvalfrdwidgvl nppgppa 225

RESULT 5

AA71891

Db	8	ivggrkarprgfplasiqngqhfncgqaliharfvmtaascfgsqngpvgstvvtvlgaydl	67
QY	61	RRRRQSRQTSISMSSENGYDPOQLNDMLQLDREANLTSSVTILPLPLQNAIVEAG	120
Db	68	rrrrrsqrqtisismseengydpqqlndmlqldreantssvtlplplqnatveag	127
QY	121	TRCOVAGSGRSQRGRLSRFRFVNVTVPEDOCRPNNVCTGVLTRRGICNGDGGTFLV	180
Db	128	trcqvagwgsrsggrlsrfrfvnvtvpdqcrpnncvctgvltrrgicngdggtplv	187
QY	181	CSGLAHGVAVSFLSPCGRGDEFFTRVALFDWIDGVLNPPGPGA	225
Db	188	ceqlahgvasfslpcgrqgdftrvalfrdwidgvlppgqpa	232

RESULT	8
AAW88364	
ID	AAW88364 standard; Protein; 232 AA.
XX	AC
XX	AAW88364;
XX	
DT	26-APR-1999 (first entry)
XX	
DE	Human pro-heparin binding protein.
XX	
XX	Heparin binding protein; HBP; human; pathogen; Mycobacterium;
KW	Listeria; Leishmania; HIV; infection; therapy; mononuclear cell;
KW	monocyte; macrophage.
OS	Homo sapiens.
XX	
XX	Key
XX	Location/Qualifiers
FT	Peptide
FT	1..7
FT	/note= "pro-peptide"
FT	Protein
FT	8..232
FT	/note= "mature HBP"
XX	
PN	WO9900416-A1.
XX	
PD	07-JAN-1999.
XX	
PD	22-JUN-1998; 98WO-DK00274.
DF	
XX	22-AUG-1997; 97DK-0000962.
PR	25-JUN-1997; 97US-0050787.
PR	30-JUN-1997; 97DK-0000772.
PR	11-AUG-1997; 97US-0055191.
XX	
XX	(NOVO) NOVO-NORDISK AS.
PA	
XX	
PL	Flodgaard HJ, Rasmussen PB;
XX	
DR	WPI; 1999-095679/08.
DR	N-PSDB; AAX06765.
XX	
XX	Inhibiting pathogen entry into mononuclear cells using
PT	heparin-binding protein - useful to treat diseases caused by
PT	intracellular pathogens e.g. Leishmania, Listeria, Mycobacterium
PT	tuberculosis or human immunodeficiency virus
XX	
XX	Disclosure; Page 30-31; 57pp; English.
PS	
XX	
CC	This polypeptide comprises human heparin binding protein (HBP)
CC	pro-peptide and mature protein. A novel method for inhibiting
CC	entry of a pathogen into mononuclear cells of a patient comprises
CC	administering a pharmaceutical composition comprising a carrier or
CC	diluent and a mammalian HBP, especially a human or porcine mature
CC	HBP (see also AAW88362-63) which, in glycosylated form: (i) has
CC	mol.wt. of approximately 28 kDa as determined by SDS-PAGE under
CC	reducing conditions; (ii) is produced in the atropophil granules of
CC	polymorphonuclear leukocytes; and (iii) is a chemottractant for
CC	monocytes. The method is useful for inhibiting the entry of
CC	pathogens such as protozoa (especially Leishmania), bacteria

XX PA (NOVO) NOVO NORDISK AS.
 XX PI Flodgaard HJ, Rasmussen PB, Bjorn S, Svendsen I;
 XX PN WPI; 2001-015973/02.
 XX PD N-PSDB; AAD01933.
 XX PF Producing mammalian heparin-binding proteins to mediate detachment and
 XX PT contraction of endothelial cells and fibroblasts, involves introducing
 XX PR genes encoding heparin-binding proteins into mammalian cells and
 XX PT culturing.
 XX PS Disclosure; Page 6; 44pp; English.
 XX PI The invention relates to a method for producing heparin-binding
 XX CC protein (HBP) in a mammalian cell that can be cultured under
 XX CC anaerobic conditions involving introducing gene encoding HBP into
 XX CC mammalian cells, culturing the cell under conditions conducive to
 XX CC expression of HBP, and recovering HBP from the culture medium. This
 XX CC method is useful for producing HBP in recombinant mammalian cells.
 XX CC The present sequence is human heparin-binding
 XX CC protein (HBP) (which includes signal sequence and mature protein).
 XX CC HBP is a proteolytically inactive protein stored in the azurophil
 XX CC granules of polymorphonuclear leukocytes. HBP functions as a
 XX CC chemoattractant for monocytes. HBP is used to mediate detachment
 XX CC and contraction of endothelial cells and fibroblasts when added to
 XX CC cells grown in monolayer cultures. It is also used to stimulate
 XX CC monocyte survival and thrombospondin secretion.
 XX SQ Sequence 244 AA;
 Query Match 100.0%; Score 1198; DB 22; Length 244;
 Best Local Similarity 100.0%; Pred. No. 4.1e-89;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVGGRKARPPFPFLASIQNGRHFCGGALIHARFVMTAASCFOSONPGVSTVVLGAYDL 60
 Db 20 ivggrkarppfpflasiqnggrhfcggaliiharfvmtaascfsgqpgvstvlvlgaydl 79
 QY 61 RRRERQSRQTSISSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAATVEAG 120
 Db 80 rrrerqsrqtssissmsengydpqgnldmlqldreanltssvtlilplqnatveag 139
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTPTDQCPRNNVCTGVLTRRGSGICNGDGGTPLV 180
 Db 140 trcqvagwsqsggrslrfrfvnvtptdqcrpnnvctgvltrrgsgicngdggtplv 199
 QY 181 CEGLAHGVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNNGPGPA 225
 Db 200 ceglahgvasfslgpcgrgdpdfttrvalfrdwidgvlnnpgpapa 244
 RESULT 11
 AAR10668
 ID AAR10668 standard; Protein; 251 AA.
 XX AC AAR10668;
 XX DT 17-APR-1991 (first entry)
 XX DE Cationic granule protein 37 sequence from clone 6a.1.
 XX KW Cationic granule protein 37; CAT37; polymorphonuclear leukocytes;
 KW PMN; lipopolysaccharide; LPS; wound healing; monocyte;
 KW chemoattractant.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= sig_peptide

FT Protein 27..251
 FT /label= mat_protein
 XX WO9100907-A.
 XX PN 24-JAN-1991.
 XX PD 03-JUL-1990; 90WO-US03772.
 XX PF 05-JUL-1989; 89US-0375739.
 XX PR (UYEM-) EMORY UNIV.
 XX PA (GENE-) GENELABS INC.
 XX PI Larrick JW, Morgan JG, Pereira HA, Spitznagel JK;
 XX WPI; 1991-051334/07.
 XX DR N-PSDB; AAQ10490.
 XX PT Recombinant DNA molecule encoding cationic granule protein -
 PT binds to Gram negative bacterial lipo:polysaccharide as monocyte
 PT chemoattractant, for treatment of wounds and monocyte disorders
 XX PS Disclosure; Page 82; 110pp; English.
 XX CC The mature form of CAP37 has an estimated mol.wt. of 24.276 kD.
 CC Previously Shafer et al. determined the mol.wt. to be 37 kD.
 CC This discrepancy is most likely the result of post-translational
 CC modification, e.g. glycosylation.
 CC The protein is a monocyte chemoattractant and can increase the
 CC migration of monocytes to a tissue site. It is therefore useful in
 CC wound healing, when used in a topical medication. It is useful for
 CC treating diseases involving monocyte localisation or defects of
 CC monocyte chemotaxis in an animal. The peptide can also be used for
 CC treating tumours of monocytes. The protein binds to bacterial LPS and
 CC therefore may provide an effective treatment for endotoxaemia.
 CC See also AAQ10490-95.
 XX SQ Sequence 251 AA;
 Query Match 100.0%; Score 1198; DB 12; Length 251;
 Best Local Similarity 100.0%; Pred. No. 4.2e-89;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IVGGRKARPPFPFLASIQNGRHFCGGALIHARFVMTAASCFOSONPGVSTVVLGAYDL 60
 Db 27 ivggrkarppfpflasiqnggrhfcggaliiharfvmtaascfsgqpgvstvlvlgaydl 86
 QY 61 RRRERQSRQTSISSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLQNAATVEAG 120
 Db 87 rrrerqsrqtssissmsengydpqgnldmlqldreanltssvtlilplqnatveag 146
 QY 121 TRCQVAGWSQSGRSLRFRFVNVTPTDQCPRNNVCTGVLTRRGSGICNGDGGTPLV 180
 Db 147 trcqvagwsqsggrslrfrfvnvtptdqcrpnnvctgvltrrgsgicngdggtplv 206
 QY 181 CEGLAHGVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNNGPGPA 225
 Db 207 ceglahgvasfslgpcgrgdpdfttrvalfrdwidgvlnnpgpapa 251
 RESULT 12
 AAR84666
 ID AAR84666 standard; Protein; 251 AA.
 XX AC AAR84666;
 XX DT 02-JUN-1996 (first entry)
 XX DE Human heparin-binding protein.
 XX KW Heparin-binding protein; Gram-negative sepsis; septic shock;

KW disseminated intravascular coagulation; meningococcal meningitis;
KW lipopolysaccharide-induced cytokine cascade; disease; prevention;
KW therapy; plasmid pKEN-1783; Spodoptera frugiperda.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /note= "signal peptide"
FT Peptide 20..26
FT Peptide /label= propeptide
FT Protein /note= "N-terminal extension"
FT Protein 27..251
FT Protein /note= "mature heparin-binding protein"
FT Protein 27..247
FT Protein /note= "heparin-binding protein of AAR84663"
XX
XX W09528949-A1.
XX
XX 02-NOV-1995.
XX
XX 17-MAR-1995; 95WO-DK00121.
XX
XX 21-DEC-1994; 94DK-0001452.
XX 21-APR-1994; 94DK-0000464.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Flodgaard HJH, Rasmussen PB;
PI N-PSDB; AAT05129.
XX
XX Heparin-binding protein (HBP) composition - for prevention and
PT treatment of sepsis and other conditions
XX
XX Disclosure; Fig 2; 48pp; English.
XX
XX The sequence represents the human heparin-binding protein (HBP)
CC which is expressed in Spodoptera frugiperda insect cells transformed
CC with plasmid pSX221. The cells are cultured in a suitable medium,
CC i.e. one containing a sulphated polysaccharide (heparin) immobilised
CC on an inert carrier (agarose), under conditions suitable for HBP
CC expression. The protein sequence represents mature HBP preceded by
CC an N-terminal extension. To facilitate production of mature HBP,
CC a preferred DNA encodes an N-terminally extended HBP including a
CC protease cleavage site located between the N-terminal extension and
CC the mature HBP coding sequence i.e. (Asp-Glu-Gly-Arg) (Factor-Xa).
CC These sequences can be engineered into the DNA sequence (protein sequence position 26-27). HBP, or its
CC fragments, are used in a pharmaceutical composition for the
CC prevention or treatment of diseases associated with induction of the
CC cytokine cascade by glycosylated lipopolysaccharide, specifically
CC Gram-negative sepsis, septic shock, disseminated intravascular
CC coagulation or meningococcal meningitis.
XX
SQ Sequence . 251 AA;

Query Match 100.0%; Score 119; DA 16; Length 251;
Best Local Similarity 100.0%; Pred. No. 2e-89;
Matches 225; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 IVGGRKARQFPFLASTNQGRHFCGGLIHAKEMTAASCFQSQNPQGVSTVVLGAYDL 60
Db 27 ivggrkarqfpflasiqgrhfcggliahermtaascfqsqnpqvstvvlgaydl 86

Qy 61 RRRRQRQRQTFSTSSSENGYDFQONLMLLQREANLTSSVILLPLPLQNATVEAG 120
Db 87 rrrrqrqrqrqtfstsssenngydfpqnlmlqlreantlssvtllplplqnatveag 146

Qy 121 TRCQVAGWSQSGRLSRPFRFVNVTVTPEDOCNNVCTGVLTTRGGICNGDGGTPLY 180
Db 121 trcqvagwsqsggrlslrfrfvnvtvtpedqcrpnnvctgvltrrgicngdggtply 206

Db 147 trcqvagwsqsggrlslrfrfvnvtvtpedqcrpnnvctgvltrrgicngdggtply 206
Qy 181 CEGLAHGVASFSLGPGCGRGPDPFTRVALFRDWIDGVLNNPQGP 225
Db 207 ceglahgvasfslgpcgrgdpfftrvalfrdwidgvlnnpgp 251

RESULT 13
AAW88365
ID AAW88365 standard; Protein; 251 AA.
XX
AC AAW88365;
XX
DT 26-APR-1999 (first entry)
XX
DE Human prepro-heparin binding protein.
XX
KW Heparin binding protein; HBP; human; pathogen; Mycobacterium;
KW Listeria; Leishmania; HIV; infection; therapy; mononuclear cell;
KW monocyte; macrophage.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /note= "signal peptide"
FT Peptide 20..26
FT Peptide /note= "pro-peptide"
FT Protein 27..251
FT Protein /note= "mature HBP"
XX
PN W09900416-A1.
XX
XX 07-JAN-1999.
XX
XX 22-JUN-1998; 98WO-DK00274.
XX
XX 22-AUG-1997; 97DK-0000962.
XX 25-JUN-1997; 97US-0050787.
XX 30-JUN-1997; 97DK-0000772.
XX 11-AUG-1997; 97US-0055191.
XX (NOVO) NOVO-NORDISK AS.
XX
XX Flodgaard HJ, Rasmussen PB;
PI N-PSDB; AAX06766.
XX
XX Inhibiting pathogen entry into mononuclear cells using
XX heparin-binding protein - useful to treat diseases caused by
XX intracellular pathogens e.g. Leishmania, Listeria, Mycobacterium
XX tuberculosis or human immunodeficiency virus
XX
XX Disclosure; Page : 57pp; English.
XX
XX This polypeptide comprises human heparin binding protein (HBP)
XX signal peptide, pro-peptide and mature protein. A novel method for
XX inhibiting entry of a pathogen into mononuclear cells of a patient
XX comprises administering a pharmaceutical composition comprising a
XX carrier or diluent and a mammalian HBP, especially a human or
XX porcine mature HBP (see also AAW88362-63) which, in glycosylated form:
XX (i) has a mol.wt. of approximately 28 kDa as determined by SDS-PAGE
XX under reducing conditions; (ii) is produced in the azurophilic granules
XX of polymorphonuclear leukocytes; and (iii) is a chemottractant for
XX monocytes. The method is useful for inhibiting the entry of
XX pathogens such as protozoa (especially Leishmania), bacteria
XX (especially Listeria or Mycobacterium e.g. Mycobacterium
XX tuberculosis) and viruses (especially HIV) into mononuclear cells,
XX especially monocytes or macrophages in humans or pigs. It may also
XX be used to treat diseases caused by intracellular pathogens.
XX (NB, the sequence of the signal and pro-peptide of human prepro-HBP
XX are not provided in the specification, but have been deduced from

CC the DNA sequence given in AAX06766).

XX Sequence 251 AA;

Query Match 100.0%; Score 1198; DB 20; Length 251;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPRQFPFLASIQNGRHFCCGALIHARFVMTAASCFSQNGPSTVVLGAYDL 60
DB 27 IVGGRKARPRQFPFLASIQNGRHFCCGALIHARFVMTAASCFSQNGPSTVVLGAYDL 86
QY 61 RRRERQSRQTSISMSSENGYDPOQNLNDMLLDREANLTSSVTILPLQNAATVEAG 120
DB 87 RRRERQSRQTSISMSSENGYDPOQNLNDMLLDREANLTSSVTILPLQNAATVEAG 146
QY 121 TRCQVAGWSQSGRLSRFPFVNVVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 180
DB 147 TRCQVAGWSQSGRLSRFPFVNVVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 206
QY 181 CEGLAGHVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNPNPGPPA 225
DB 207 CEGLAGHVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNPNPGPPA 251

RESULT 14

AAAY71878
ID AAY71878 standard; Protein; 251 AA.

XX AAY71878;

XX 26-MAR-2001 (first entry)

XX Human pre-pro heparin binding protein (HBP).

XX Human; heparin binding protein; HBP; antiinflammatory; cardiovascular;
XX immunosuppressive; vasotropic; prevention; treatment; bradykinin;
XX aprotinin; H-kininogen; systemic inflammatory response syndrome;
XX pre-kallikrein; ischaemia reperfusion; anaphylaxis; allograft rejection;
XX adult respiratory distress syndrome; chemoattractant; inflammation;
XX vascular damage.

XX Homo sapiens.

XX WO200066151-A1.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-DK00213.

XX 29-APR-1999; 99US-0132748.

XX 06-MAY-1999; 99DK-0000613.

XX 01-OCT-1999; 99DK-0001402.

XX 01-OCT-1999; 99US-0157384.

XX (NOVO) NOVO NORDISK AS.

XX Flodgaard HJ; Lindbom L, Bjorn S;

XX WPI: 2000-687445/67.

XX N-PSDB; AAD01924.

XX Treating systemic inflammatory response syndrome, ischaemia reperfusion,
XX anaphylaxis and allograft rejection by modulating release of bradykinin

XX Disclosure; Page 13; 75pp; English.

XX The present sequence is a human pre-pro heparin binding protein (HBP)
XX which contains a pro sequence, a signal sequence and a mature HBP
XX sequence. HBP is a proteolytically inactive protein and is stored in
XX the azurophil granules of polymorphonuclear leucocytes. It induces

CC contraction in the endothelial cells and fibroblasts. It serves as
CC a chemoattractant for monocytes and/or activates them and is involved
CC in the progression of inflammation. HBP serves as the signalling link
CC in neutrophil induced vascular damage and activation of contact phase
CC system with concomitant formation of bradykinin. It specifically plays a
CC role in the pre-kallikrein (PK) mediated cleavage of bradykinin. It
CC obtain the bradykinin sequence. The antagonists of HBP (e.g. aprotinin)
CC decrease the permeability of the endothelial cells and are used to
CC prevent or treat disorders resulting from the release of bradykinin
CC such as systemic inflammatory response syndrome, ischaemia reperfusion,
CC anaphylaxis and/or allograft rejection. They are also used to treat
CC adult respiratory distress syndrome.

XX Sequence 251 AA;

Query Match 100.0%; Score 1198; DB 21; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPRQFPFLASIQNGRHFCCGALIHARFVMTAASCFSQNGPSTVVLGAYDL 60
DB 27 IVGGRKARPRQFPFLASIQNGRHFCCGALIHARFVMTAASCFSQNGPSTVVLGAYDL 86
QY 61 RRRERQSRQTSISMSSENGYDPOQNLNDMLLDREANLTSSVTILPLQNAATVEAG 120
DB 87 RRRERQSRQTSISMSSENGYDPOQNLNDMLLDREANLTSSVTILPLQNAATVEAG 146
QY 121 TRCQVAGWSQSGRLSRFPFVNVVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 180
DB 147 TRCQVAGWSQSGRLSRFPFVNVVTPEDQCRPNNVCTGVLTTRGGICNGDGGTPLV 206
QY 181 CEGLAGHVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNPNPGPPA 225
DB 207 CEGLAGHVASFSLGPGCGRGPDEFTRVALFRDWIDGVLNPNPGPPA 251

RESULT 15

AAAY71894

ID AAY71894 standard; Protein; 251 AA.

XX AAY71894;

XX 26-MAR-2001 (first entry)

XX Human preproheparin-binding protein (HBP).

XX Human; heparin-binding protein; HBP; chemoattractant; monocyte;
XX thrombospondin; fibroblast; endothelial cell.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..19

XX /label= Signal_peptide

XX Region 20..26

XX /note= "Pro-sequence of heparin-binding protein"

XX Protein 27..251

XX /label= Mature_heparin_binding_protein

XX WO200066627-A1.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-DK00216.

XX 29-APR-1999; 99US-0131574.

XX 06-MAY-1999; 99DK-0000612.

XX (NOVO) NOVO NORDISK AS.

XX Flodgaard HJ, Rasmussen PB, Bjorn S, Svendsen I;

XX

DR WPI: 2001-015973/02.
DR N-PSDB; AAD01934.
XX
XX Producing mammalian heparin-binding proteins to mediate detachment and
PT contraction of endothelial cells and fibroblasts, involves introducing
PT genes encoding heparin-binding proteins into mammalian cells and
PT culturing -
XX
XX Disclosure; Page 7; 44pp; English.
PS
XX The invention relates to a method for producing heparin-binding
CC protein (HBP) in a mammalian cell that can be cultured under
CC anaerobic conditions involves introducing a gene encoding HBP into
CC mammalian cells, culturing the cell under conditions conducive to
CC expression of HBP, and recovering HBP from the culture medium. This
CC method is useful for producing HBP in recombinant mammalian cells.
CC The present sequence is human heparin-binding protein (HBP) which
CC protein (HBP) (which includes signal sequence, the pro sequence
CC and sequence of the mature protein).
CC HBP is a proteolytically inactive protein stored in the azurophil
CC granules of polymorphonuclear leucocytes. HBP functions as a
CC chemoattractant for monocytes. HBP is used to mediate detachment
CC and contraction of endothelial cells and fibroblasts when added to
CC cells grown in monolayer cultures. It is also used to stimulate
CC monocyte survival and thrombospondin secretion.
XX
XX Sequence 251 AA;
SQ

Query Match 100.0%; Score 119; DB 22; Length 251;
Best Local Similarity 100.0%; Pred. No. 2e-89;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IVGGRKARPRQFFFLASIQNGRHFCGGALIHARMTAASCFOSONPGVSTVILGAYDL 60
DB 27 ivggrkarprqffflasiqngqrhfcggaliharmtaascfqsqnpqgvstvigaydl 86
QY 61 RRRERQSRQTFSTSSMSSENGYDPOQNLNDLMLIQREANLTSSVTILPLQONATVEAG 120
DB 87 rrrerqsrqtfstssmsengydpqgnlndlmlqreantlssvtilplqnatveag 146
QY 121 TRCOVAGWSQSGRLSRFRFVNVTVPEDOCNNVCTGVLTTRGGICNGDGGTPLY 180
DB 147 trcvagwsgsggrlsrfrfvnvtvpedqcnnvctgvlttrggicngdggtply 206
QY 181 CEGLAHGVASFSLGCGRGPDFFTRVALFRDWIDVLNNPGPGPA 225
DB 207 ceglahgvasfslgpcgrgpdfftrvalfrwdvlinnpgpgpa 251

Search completed: November 23, 2001, 06:11:3
Job time: 53 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2001, 07:18:06 ; Search time 12.57 Seconds
(without alignments)
402.804 Million cell updates/sec

Title: US-09-559-764-1
Perfect score: 1198
Sequence: 1 IVGGRKARPRQPFPLASTQN.....VALFRDWTGVLNPNPGGPA 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues
number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1198	100.0	225	4	US-08-944-483-32
2	1181	98.6	222	1	US-07-969-931-9
3	1181	98.6	222	1	US-07-855-417A-9
4	1176	98.2	222	2	US-08-491-204A-18
5	1161	96.9	221	2	US-08-925-708-1
6	766	63.9	219	2	US-08-925-708-2
7	500	41.7	238	4	US-08-944-483-31
8	500	41.7	238	6	5180819-4
9	500	41.7	267	2	US-08-978-404B-46
10	476.5	39.8	229	2	US-08-394-600B-20
11	476.5	39.8	229	4	US-08-944-483-30
12	476.5	39.8	229	5	PCT-US95-02513-20
13	476.5	39.8	256	2	US-08-230-428B-4
14	434	36.2	214	6	5180819-3
15	417.5	34.8	215	6	5180819-2
16	333	27.8	234	4	US-08-944-483-46
17	331	27.6	224	1	US-08-278-091-12
18	331	27.6	224	1	US-08-483-859-12
19	331	27.6	224	1	US-08-472-173-12
20	331	27.6	224	2	US-08-487-167-12
21	331	27.6	224	2	US-08-482-816-12
22	331	27.6	224	2	US-08-296-149-12
23	331	27.6	224	2	US-08-801-499-12
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27	331	27.6	224	3	US-09-106-468-12

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30 331 27.6 247 2 US-08-978-404B-47
31 329.5 27.5 232 4 US-08-944-483-45
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44 314.5 26.3 222 6 5223425-6
45 309 25.8 248 2 US-08-851-974-3

ALIGNMENTS

RESULT 1
US-08-944-483-32
; Sequence 32, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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Sequence 47, Appl
Sequence 45, Appl
Patent No. 5223425
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Patent No. 5223425
Sequence 44, Appl
Patent No. 5223425
Patent No. 5223425
Sequence 14, Appl
Sequence 14, Appl
Sequence 42, Appl
Sequence 14, Appl
Sequence 41, Appl
Patent No. 5223425
Sequence 3, Appl

; MOLECULE TYPE: No. 6232456e
US-08-944-483-32

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Qy 61	RRRERQSRQTFSSISMSENGYDPOONLNDMLLQ	FEANLTSVTLILPLQNATVEAG 120		
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Query Match          98.6%; Score 1181; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.5e-116;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1  IVGSKARPRQFPFLASIQNGRHFCCGALIHARFVMTAAACFQSONPGVSTVVLGAYDL 60
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      61  RRRERQSRQTSFSSMSSENGYDPOONLNDMLQLDREANLTSSVTILPLQNATVEAG 120
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      61  RRRERQSRQTSFSSMSSENGYDPOONLNDMLQLDREANLTSSVTILPLQNATVEAG 120
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      121  TRCOVAGWGSGRSLRPRFVNVVITPDDQCRPNNVCTGVLTRGGTCNGDGGTPLY 180
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DB      121  TRCOVAGWGSGRSLRPRFVNVVITPDDQCRPNNVCTGVLTRGGTCNGDGGTPLY 180
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QY      181  CEGLAHGVAVSFLGPCRGKGPDDFTFRVALFRDWIDGVLNNPGP 222
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DB      181  CEGLAHGVAVSFLGPCRGKGPDDFTFRVALFRDWIDGVLNNPGP 222
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RESULT      3
US-07-855-417A-9
; Sequence 9, Application US/07855417A
; Patent No. 5484885
; GENERAL INFORMATION:
; APPLICANT: Pereira, Heloise Anne
; APPLICANT: Spitznagel, John K.
; TITLE OF INVENTION: Chemotactic, Antibiotic and
; TITLE OF INVENTION: Lipopolysaccharide-Binding Peptide Fragments of CAP37
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: 133 Carnegie Way N.W., Suite 400
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/855,417A
; FILING DATE: 18-MAR-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/543,151
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/375,739
; FILING DATE: 05-JUL-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Severson, Mary L.
; REGISTRATION NUMBER: 34,927
; REFERENCE/DOCKET NUMBER: 0510.024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-07-855-417A-9

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Query Match 98.6%; Score 1181; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.5e-116;

Matches' 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 IVGGRKARPPFPFLASIQNGRHFCGCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
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QY 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
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Db 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
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QY 121 TRCQVAGWSQSRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180
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Db 121 TRCQVAGWSQSRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180
|||||
QY 181 CEGLAGHVASFSLGPGCGRPDFFTRVALFRDWIDGVLNNPGP 222
|||||
Db 181 CEGLAGHVASFSLGPGCGRPDFFTRVALFRDWIDGVLNNPGP 222
|||||

RESULT 5
US-08-925-708-1
; Sequence 1, Application US/08925708
; Patent No. 5939390
; GENERAL INFORMATION:
; APPLICANT: Fiodgaard, Hans
; APPLICANT: Rasmussen, Poul Baad
; TITLE OF INVENTION: A Pharmaceutical Composition
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5939390o No. 5939390disk of No. 5939390th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925.708
; FILING DATE: 9-SEPT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Aglis, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4319.204-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 221 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: human
; US-08-925-708-1

Query Match 96.9%; Score 1161; DB 2; Length 221;
Best Local Similarity 98.2%; Pred. No. 1.8e-114;
Matches 217; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IVGGRKARPPFPFLASIQNGRHFCGCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
|||||
Db 1 IVGGRKARPPFPFLASIQNGRHFCGCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
|||||
QY 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
|||||
Db 61 RRRERQSRQTFSSMSSENGYDPOQNLNDMLQLDREANLTSSVTILPLPLQNAATVEAG 120
|||||
QY 121 TRCQVAGWSQSRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180
|||||
Db 121 TRCQVAGWSQSRGRLSRFRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLY 180
|||||
QY 181 CEGLAGHVASFSLGPGCGRPDFFTRVALFRDWIDGVLNNPGP 222
|||||
Db 181 CEGLAGHVASFSLGPGCGRPDFFTRVALFRDWIDGVLNNPGP 222
|||||

US-08-491-204A-18
; Sequence 18, Application US/08491204A
; Patent No. 5837247
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Joost B.
; APPLICANT: Chertov, Oleg
; APPLICANT: Michael, Dennis F.
; APPLICANT: Xu, Luoling
; APPLICANT: Wang, Ji Ming
; APPLICANT: Murphy, William J.
; APPLICANT: Longo, Dan L.
; APPLICANT: Taub, Dennis D.
; TITLE OF INVENTION: CHEMOTACTIC AGENTS FOR T-CELLS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491.204A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15260
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-491-204A-18

Query Match 98.2%; Score 1176; DB 2; Length 222;
Best Local Similarity 99.5%; Pred. No. 4.9e-116;
Matches 221; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IVGGRKARPPFPFLASIQNGRHFCGCGALIHARFVMTAAASCFQSONPGVSTVVLGAYDL 60
|||||

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Db 121 TRCQVAGWSQSGRLSRPFBVTVTPEDOCNNVCTGLTRRGICNGDGGTPLV 180
QY 181 CEGLAGHVASFSLGPCRGDPDFTRVALFRDWIDNNPG 221
Db 181 CEGLAGHVASFSLGPCRGDPDFTRVALFRDWIDNNPG 221

RESULT 6
US-08-925-708-2
; Sequence 2, Application US/08925708
; Patent No. 5939390
; GENERAL INFORMATION:
; APPLICANT: Flogdaard, Hans
; APPLICANT: Rasmussen, Poul Baad
; TITLE OF INVENTION: A Pharmaceutical Composition
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59393900 No. 59393900 of No. 5939390th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,708
; FILING DATE: 9-SEPT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4319, 204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: porcine
; US-925-708-2

Query Match 63.9%; Score 766; DB 2; Length 219;
Best Local Similarity 67.7%; Pred. No. 2e-73;
Matches 149; Conservative 41; Indels 2; Gaps 2;

QY 1 IVGGRKARPPFPFLASIQNGRHFCGCGALIHAFVMTAASCFSQNGPVGSTVVLGAYDL 60
Db 1 IVGGRRAQPEPFLASIQNGRHFCGCGALVHPVMTAASCFCRGKSGSASVVLGAYDL 60
QY 61 RRREROSRQTSISSMSSENGYDPOONLNDMLLDREANLTSSVTILPLQNATVEAG 120
Db 61 RQOE-QSRQTSIRSIQSGYDPRQNLNDVLLQDREARLTSPVALVPLPPQBATVEAG 119
QY 121 TRCQVAGWSQSGRLSRPFBVTVTPEDOCNNVCTGLTRRGICNGDGGTPLV 180
Db 120 TNCQVAGWGTQRLRLFSRFPVLVTVT-SNPDMDICIGVFSRRGIRISQGRGTPLV 178
QY 181 CEGLAGHVASFSLGPCRGDPDFTRVALFRDWIDNNPG 220
Db 179 CNGLAGVASFSLRRFRSSGFFTRVALFRDWIDNNPG 218

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RESULT 7
US-08-944-483-31
; Sequence 31, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183-US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
; US-08-944-483-31

Query Match 41.7%; Score 500; DB 4; Length 238;
Best Local Similarity 45.2%; Pred. No. 6.5e-45;
Matches 104; Conservative 36; Mismatches 82; Indels 8; Gaps 4;

QY 1 IVGGRKARPPFPFLASIQNGRHFCGCGALIHAFVMTAASCFSQNGPVGSTVVLGAYDL 60
Db 1 IVGGRRAQPEPFLASIQNGRHFCGCGALVHPVMTAASCFCRGKSGSASVVLGAYDL 60
QY 61 RRREROSRQTSISSMSSENGYDPOONLNDMLLDREANLTSSVTILPLQNATVEAG 120
Db 61 SRRE-PTROQFAVORIFENGIDYDVLNDIVILQNGSATINANVQVQALPAQRLNG 119
QY 121 TRCQVAGWSQSGRLSRPFBVTVTPEDOCNNVCTGLTRRGICNGDGGTPLV 180
Db 120 VQCLANGWGLLGRNGIASVLQELNVTV-TSLCRRSNVCTILVRGQAGVCFDGSPLV 178
QY 181 CEGLAGHVASFSLGPCRG--PDFFTRVALFRDWIDVL----NNPQGP 224
Db 179 CNGLIHGIASFVRGGCASGLYPDAFAPVQFVNWIDSIITORSDDNCPHP 228

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Query Match 41.7%; Score 500; DB 2; Length 267;
Best Local Similarity 45.2%; Pred. No. 7.5e-45;
Matches 104; Conservative 36; Mismatches 82; Indels

Db	30	IVGRRARPHAWPMVSLQURGGHFCGATLIAFNFM3AAHCVANVNVRVRYVVLGAHNL 89
QY	61	RRREQRQSTSTSSMSGSDYDQOQLNDMLLQLDREANLTSSVTILPLQLQNAIVEAG 120
Db	90	SRRE-PTTQVFAVORIENGSDYDPNLLDIVILQLNGSATNANVQVAQIPLAQRRLGNG 148
QY	121	TRCQVAGMSQRSGRLSRFRFVNVTPTPEDQRPNNVCTGVLTRRGICNGSDGGTPLY 180
Db	149	VQCLAMGWGLLRNRGIASVLQELNVTV--TSLCRSRNVCTLVLRGRQAGVCFGSDGSPLY 207
QY	181	CBGLAHGVAASFLGPCGRG--PDEFTFVALFRDWIDGVL----NNPGGP 224
Db	208	CNGLTHGTASVRRGCGASGLYPAFAVPAQVFNWIDSIORSEDNPCPH 257

APPLICANT: Harenbeck, Robert F.
 APPLICANT: Jewell, David A.
 APPLICANT: Koths, Kirston E.
 APPLICANT: Kriegel, Michael
 APPLICANT: Perez, Carl
 TITLE OF INVENTION: Compositions for the Inhibition of
 TITLE OF INVENTION: Protein Hormone Formation and Uses Thereof
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street; 34th Floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/394,600B
 FILING DATE: 02/27/95
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Donald J. Pochoplen
 REGISTRATION NUMBER: 32,167
 REFERENCE/DOCKET NUMBER: 820.005/11850US05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX:
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 229 amino acids
 TYPE: amino acid

FCI-US93-02313-20

Query Match 39.8%; Score 476.5; DB 5; Length 229;
Best Local Similarity 44.6%; Pred. No. 1.8e-42;
Matches 99; Conservative 40; Mismatches 76; Indels 7; Gaps 4;

QY 1 IVGGRKARPPFPFLASIQ---NOGRHFCGGALIHAREVMTAASCFSQNPQGVSTVVLGA 57
DB 1 IVGGHEAQPSPRYMASLQMRGNPGSHFCGGTLIHPSFVLTAACHLRDIPQRLNVNVLGA 60

QY 58 YLRRERQSRQTSISSMSSENGYDQONLNDMLLQLDREANLTSVITLPLPLQNAV 117
DB 61 HNVRTQE-PTQOHFSAQVFLNNYDAENKLDVLLIQLSSPANLSASVATVQLPQDQPV 119

QY 118 EAGTRCOVAGWSQSGRLSRFPFVNVTVPEDCRPNNVCTGVLTRGGICNGDGGT 177
DB 120 PHGTCLAMGWGRVGAHPDPAQVQLQELNVTV-TFFCRPHNICTFVPRKAGICFGDGG 178

QY 178 PLVCEGLAHGVASFSLGPGCRG--PDFFTRVALFRDWIDGVL 217
DB 179 PLICDGLIIGDSFVWGCATRLFPDFFTRVALYVDWIRSTL 220

RESULT 13
US-08-230-428B-4
; Sequence 4, Application US/08230428B
; Patent No. 5998378
; GENERAL INFORMATION:
; APPLICANT: Krieglner, Michael
; APPLICANT: Perez, Carl
; APPLICANT: Halenbeck, Robert F.
; APPLICANT: Jewell, David A.
; APPLICANT: Koths, Kirston E.
; TITLE OF INVENTION: Compositions For The Inhibition Of TNF
; TITLE OF INVENTION: Hormone Formation And Uses Thereof (As Amended)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION Intellectual Property - R440
; STREET: 4560 Horton Street, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: United States of America
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,428B
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,546
; FILING DATE: 25-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/395,253
; FILING DATE: 16-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0820.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-230-428B-4

Query Match 39.8%; Score 476.5; DB 2; Length 256;
Best Local Similarity 44.6%; Pred. No. 2.1e-42;
Matches 99; Conservative 40; Mismatches 76; Indels 7; Gaps 4;

QY 1 IVGGRKARPPFPFLASIQ---NOGRHFCGGALIHAREVMTAASCFSQNPQGVSTVVLGA 57
DB 28 IVGGHEAQPSPRYMASLQMRGNPGSHFCGGTLIHPSFVLTAACHLRDIPQRLNVNVLGA 87

QY 58 YLRRERQSRQTSISSMSSENGYDQONLNDMLLQLDREANLTSVITLPLPLQNAV 117
DB 88 HNVRTQE-PTQOHFSAQVFLNNYDAENKLDVLLIQLSSPANLSASVATVQLPQDQPV 146

QY 118 EAGTRCOVAGWSQSGRLSRFPFVNVTVPEDCRPNNVCTGVLTRGGICNGDGGT 177
DB 147 PHGTCLAMGWGRVGAHPDPAQVQLQELNVTV-TFFCRPHNICTFVPRKAGICFGDGG 205

QY 178 PLVCEGLAHGVASFSLGPGCRG--PDFFTRVALFRDWIDGVL 217
DB 206 PLICDGLIIGDSFVWGCATRLFPDFFTRVALYVDWIRSTL 247

RESULT 14
5180819-3
; Patent No. 5180819
; APPLICANT: CAYRE, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455,614
; FILING DATE: 22-DEC-1989
; SEQ ID NO:3
; LENGTH: 214
5180819-3

Query Match 36.2%; Score 434; DB 6; Length 214;
Best Local Similarity 44.9%; Pred. No. 4.9e-38;
Matches 93; Conservative 36; Mismatches 72; Indels 6; Gaps 4;

QY 15 LASIQ---NOGRHFCGGALIHAREVMTAASCFSQNPQGVSTVVLGAYDLRRRERQSRQT 71
DB 1 MASLQMRGNPGSHFCGGTLIHPSFVLTAACHLRDIPQRLNVNVLGAHNVRTQE-PTQOHF 59

QY 72 SISSMSSENGYDQONLNDMLLQLDREANLTSVITLPLPLQNAVTEAGTRCOVAGWSQ 131
DB 60 SVAQVFLNNYDAENKLDVLLIQLSSPANLSASVATVQLPQDQPVPHGTQCLAMGWGRV 119

QY 132 RSGGRLSRFPFVNVTVPEDCRPNNVCTGVLTRGGICNGDGGTGPLVCEGLAHGVASF 191
DB 120 GHADPPAQVQLQELNVTV-TFFCRPHNICTFVPRKAGICFGDGGGLICDGIQDGSF 178

QY 192 SLGPCGR-GPDEFFTRVALFRDWIDGVL 217
DB 179 IWGCATRLFPDFFTRVALYVDWIRSTL 205

RESULT 15
5180819-2
; Patent No. 5180819
; APPLICANT: CAYRE, YVON
; TITLE OF INVENTION: PURIFIED MYELOBLASTIN, NUCLEIC ACID
; MOLECULE ENCODING SAME, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/455,614
; FILING DATE: 22-DEC-1989
; SEQ ID NO:2
; LENGTH: 215
5180819-2

Query Match 34.8%; Score 417.5; DB 6; Length 215;

Best Local Similarity 43.3%; Pred. No. 7e-36;
Matches 90; Conservative 37; Mismatches 74; Indels 7; Gaps 4;

QY 15 LASIQ---NQRHFCGALIHARFVMTAASCPS PGYSTVVLGAYDLRREROSRQIF 71
Db :||:| | ||| ||| ||:|||| | :|| |
1 MASLOMRENPESHCEETLIHPSFVLTAACHLDR QRLVNVVLGAHNVRTQE-PTQOHF 59
QY 72 SISMSSENGYDPOONLNDMLLDREANLTSSV LPLPLQNAATVEAGTRCQVAGWGSO 131
Db |::: | ||: |||::||| |||:|||| :|| | | ||:| |||
60 SVAQVFLNNYDAENKLNLDILLIOLSSPANLSASV VQLPQODQPVPHGTCQCLAMGGRV 119
QY 132 RSGGRLSRFRFRFVNVTVTPEDQCRPNNVCTGVLT AGGICNGDGGTPLVCEGLAHGVASF 191
Db : : : |||| |||:|||| | |||| | ||:| | : ||
120 GAHDPPAQVLQELNVTW-TFFCRPHNICTFVPR AGICFGDSGGPLICDGIQIDSF 178
QY 192 SLGPCGRG--PDFFTRVALFRDWIDGVL 217
Db : | ||||||||: ||| |
179 VINGCATRLFPDFFTRVALYVDWIRSTL 206

Search completed: November 23, 2001, 07:18:23
Job time: 22 sec